

SCORE Search Results D

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This page gives you Search Results detail for the Application 10553669 and Search Result 20070620_142246_us-

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 20, 2007, 14:26:44 ; Search time 31 Seconds
(without alignments)
884.573 Million cell updates/sec

Title: US-10-553-669-3
Perfect score: 1515
Sequence: 1 PCPGACVCYNEPKVTTSCPQ.....QRLAGRDLKRLAANDLQGCA 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	342.5	22.6	605	2	A41915	insulin-like growt
2	330	21.8	1531	2	T42218	slit-1 protein hom
3	329	21.7	1523	2	T13953	MEGF5 protein - ra
4	328.5	21.7	605	2	JC5239	insulin-like growt
5	325	21.5	1469	2	B36665	slit protein 2 pre
6	325	21.5	1480	2	A36665	slit protein 1 pre
7	318.5	21.0	622	2	JC7973	synleurin - human
8	305	20.1	603	2	JC6128	insulin-like growt
9	304.5	20.1	361	2	A53860	chondroadherin pre
10	297	19.6	603	2	JC1282	insulin-like growt
11	295	19.5	907	2	JG0193	G protein-coupled

12	290	19.1	907	2	JE0176	orphan G protein-c
13	289.5	19.1	560	2	A60164	platelet membrane
14	287	18.9	536	2	A34901	lysine carboxypept
15	276.5	18.3	420	2	A53531	oncofetal trophobl
16	276	18.2	1091	2	A58532	glial cell membran
17	261	17.2	312	1	NBHUA2	leucine-rich alpha
18	250.5	16.5	707	2	JC7763	neuronal leucine-r
19	246.5	16.3	359	1	NBHUC8	decorin precursor
20	241	15.9	1025	2	T42626	secreted leucine-r
21	238.5	15.7	357	2	S24317	decorin precursor
22	234.5	15.5	682	2	A49121	cell-surface molec
23	234.5	15.5	682	2	A43318	connectin precurs
24	233.5	15.4	360	2	S06280	decorin precursor
25	230.5	15.2	360	2	I47020	decorin - rabbit
26	230	15.2	789	2	T28714	hypothetical prote
27	230	15.2	1355	2	T28715	hypothetical prote
28	227	15.0	333	2	T34555	hypothetical prote
29	226	14.9	594	2	T23841	hypothetical prote
30	226	14.9	1389	2	T13852	gene wheeler prote
31	223	14.7	1385	2	T13887	tlr protein - frui
32	221.5	14.6	354	2	A55454	decorin precursor
33	219.5	14.5	1535	2	S46224	peroxidase - frui
34	218	14.4	610	2	T23836	hypothetical prote
35	215.5	14.2	354	2	S29145	decorin precursor
36	208	13.7	382	2	I39068	proline- arginine-
37	206	13.6	1112	2	T10504	disease resistance
38	205.5	13.6	1066	2	T15864	hypothetical prote
39	204	13.5	738	2	T19938	hypothetical prote
40	202	13.3	342	2	A46743	lumican precursor
41	202	13.3	562	2	T34319	hypothetical prote
42	202	13.3	662	2	S42799	garp precursor - h
43	199.5	13.2	626	1	NBHUIA	platelet glycoprot
44	199	13.1	338	2	S52284	lumicon, secretory
45	197.5	13.0	961	2	T23395	hypothetical prote

ALIGNMENTS

RESULT 1

A41915

insulin-like growth factor-binding complex acid-labile chain precursor - human

N;Alternate names: Acid-Labile Subunit (ALS)

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: A41915

R;Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.

Mol. Endocrinol. 6, 870-876, 1992

A;Title: Structure and functional expression of the acid-labile subunit of the insulin-like growth

A;Reference number: A41915; MUID:92357025; PMID:1379671

A;Accession: A41915

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-605 <LEO>

A;Cross-references: UNIPROT:P35858; UNIPARC:UPI000000088A; GB:M86826; NID:g184807; PIDN:AAA36047.1;

A;Experimental source: liver

A;Note: sequence extracted from NCBI backbone (NCBIP:110171)

F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

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44	199	13.1	338	2	S52284	lumicon, secretory
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ALIGNMENTS

RESULT 1

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C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: A41915

R;Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.

Mol. Endocrinol. 6, 870-876, 1992

A;Title: Structure and functional expression of the acid-labile subunit of the insulin-like growth

A;Reference number: A41915; MUID:92357025; PMID:1379671

A;Accession: A41915

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-605 <LEO>

A;Cross-references: UNIPROT:P35858; UNIPARC:UPI000000088A; GB:M86826; NID:g184807; PIDN:AAA36047.1;

A;Experimental source: liver

A;Note: sequence extracted from NCBI backbone (NCBIP:110171)

F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

SCORE Search Results Details for Application 10553669
and Search Result 20070620_142244_us-10-553-669-
3.rup.

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This page gives you Search Results detail for the Application 10553669 and Search Result 20070620_142244_us-10-553-669-3.rup.

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OM protein - protein search, using sw model

Run on: June 20, 2007, 14:23:40 ; Search time 349 Seconds
(without alignments)
875.517 Million cell updates/sec

Title: US-10-553-669-3
Perfect score: 1515
Sequence: 1 PCPGACVCYNEPKVTTSCPQ.....QRLAGRDLKRLAANDLQGCA 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result		Query						
No.	Score	Match	Length	DB	ID	Description		
1	1515	100.0	473	1	RTN4R_HUMAN	Q9bzr6 homo sapien		
2	1493	98.5	473	1	RTN4R_MACFA	Q9n0e3 macaca fasc		
3	1395	92.1	473	1	RTN4R_MOUSE	Q99pi8 mus musculu		
4	1391	91.8	473	1	RTN4R_RAT	Q99m75 rattus norv		
5	910	60.1	479	2	Q6DH76_BRARE	Q6dh76 brachydanio		
6	910	60.1	479	2	Q6X3Y5_BRARE	Q6x3y5 brachydanio		
7	774.5	51.1	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n		
8	773.5	51.1	478	2	Q6WZD2_BRARE	Q6wzd2 brachydanio		

9	771.5	50.9	420	1	R4RL2_MOUSE	Q7m6z0	mus musculu
10	770.5	50.9	420	1	R4RL2_HUMAN	Q86un3	homo sapien
11	770.5	50.9	420	2	Q17RL9_HUMAN	Q17rl9	homo sapien
12	768.5	50.7	420	1	R4RL2_RAT	Q80wd1	rattus norv
13	761.5	50.3	441	1	R4RL1_HUMAN	Q86un2	homo sapien
14	755.5	49.9	457	2	Q6WZD1_BRARE	Q6wzd1	brachydanio
15	749.5	49.5	310	2	Q4RRQ4_TETNG	Q4rrq4	tetraodon n
16	748.5	49.4	445	1	R4RL1_MOUSE	Q8k0s5	mus musculu
17	745.5	49.2	445	1	R4RL1_RAT	Q80wd0	rattus norv
18	705	46.5	324	2	Q4S3K9_TETNG	Q4s3k9	tetraodon n
19	691.5	45.6	411	2	Q4S6L6_TETNG	Q4s6l6	tetraodon n
20	672.5	44.4	458	2	Q6WZD3_BRARE	Q6wzd3	brachydanio
21	373	24.6	466	2	Q66IW3_XENLA	Q66iw3	xenopus lae
22	372	24.6	411	2	Q4S9P3_TETNG	Q4s9p3	tetraodon n
23	371.5	24.5	762	2	Q5JY13_HUMAN	Q5jy13	homo sapien
24	371.5	24.5	778	2	Q6NUI6_HUMAN	Q6nui6	homo sapien
25	364.5	24.1	692	2	Q4G0S0_HUMAN	Q4g0s0	homo sapien
26	362.5	23.9	481	1	NYX_HUMAN	Q9gzu5	homo sapien
27	362.5	23.9	481	2	Q2M1S4_HUMAN	Q2m1s4	homo sapien
28	358.5	23.7	453	2	Q86XY1_HUMAN	Q86xy1	homo sapien
29	354	23.4	935	2	Q4SBT7_TETNG	Q4sbt7	tetraodon n
30	352	23.2	339	2	Q4SU68_TETNG	Q4su68	tetraodon n
31	352	23.2	417	2	Q6E4J7_PETMA	Q6e4j7	petromyzon
32	351.5	23.2	652	2	Q45R42_RAT	Q45r42	rattus norv
33	351	23.2	606	2	Q1KS52_PIG	Q1ks52	sus scrofa
34	349.5	23.1	476	1	NYX_MOUSE	P83503	mus musculu
35	349.5	23.1	652	1	LRR4_MOUSE	Q99ph1	mus musculu
36	349.5	23.1	653	1	LRR4_HUMAN	Q9hbw1	homo sapien
37	346.5	22.9	597	2	Q3I0Y3_BOVIN	Q3i0y3	bos taurus
38	346.5	22.9	602	2	Q58CS0_BOVIN	Q58cs0	bos taurus
39	345.5	22.8	640	2	Q4JIW0_HUMAN	Q4jiw0	homo sapien
40	343.5	22.7	605	2	Q8TAY0_HUMAN	Q8tay0	homo sapien
41	343.5	22.7	640	1	NGL1_HUMAN	Q9hcj2	homo sapien
42	343.5	22.7	640	1	NGL1_MOUSE	Q8c031	mus musculu
43	343.5	22.7	640	2	Q505E5_MOUSE	Q505e5	mus musculu
44	342.5	22.6	605	1	ALS_HUMAN	P35858	homo sapien
45	341.5	22.5	368	2	Q32QP3_EPTST	Q32qp3	eptatretus

ALIGNMENTS

RESULT 1

RTN4R_HUMAN

ID RTN4R_HUMAN STANDARD; PRT; 473 AA.

AC Q9BZR6;

DT 25-NOV-2002, integrated into UniProtKB/Swiss-Prot.

DT 01-JUN-2001, sequence version 1.

DT 27-JUN-2006, entry version 54.

DE Reticulon-4 receptor precursor (Nogo receptor) (NgR) (Nogo-66 receptor).

GN Name=RTN4R; Synonyms=NOGOR; ORFNames=UNQ330/PRO526;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

OC Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RC TISSUE=Brain;

RX MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;

RA Fournier A.E., GrandPre T., Strittmatter S.M.;

RT "Identification of a receptor mediating Nogo-66 inhibition of axonal

RT regeneration.";

RL Nature 409:341-346(2001).

	Ref #	Hits	Search Text
1	S1	1	("20070065429").PN.
2	S2	1	("20060058223").PN.
3	S3	0	("200019210").PN.
4	S4	1	("2000019210").PN.
5	S5	2	("0019210").PN.
6	S6	125	audia-james-e.in.
7	S7	57	audia-james-e.in. and beta-amyloid
8	S8	1	("20020077295").PN.
9	S9	8	nogo receptor polypeptide
10	S10	2	nogo receptor polypeptide and (Amyloid-beta)
11	S11	5	nogo receptor polypeptide and alzheimer's
12	S12	3	nogo receptor peptide and alzheimer's
13	S13	13	NGR1 and alzheimer's
14	S15	12	S14 and alzheimer's
15	S14	29	((Nogo adj receptor) or NogoR or NogoR-1 or NgR or NgR-1) adj antagonist
16	S16	6	"2004014311"
17	S17	1	"7029874"
18	S18	7	((("7019124") or ("7019115") or ("6974696") or ("6972325") or ("6962797") or ("6916648") or ("6812339"))).PN.
19	S19	1	("20050271655").PN.
20	S20	1	("20020012965").PN.
21	S21	1	("7118165").PN.
22	S22	1	("7119165").PN.
23	S23	4	Relton-j-k-.in.
24	S24	5	"2005059515"
25	S25	6	"2004014311"
26	S26	5	"2004093893"
27	S27	1	("7195760").PN.
28	S28	1	("2000053758").PN.
29	S29	0	("200053758").PN.
30	S30	0	("200053758").PN.
31	S31	2	("0053758").PN.
32	S32	6	WO200053758
33	S33	16	"200053758"
34	S34	3	"6627741"
35	S35	1	"7029874"

	Ref #	Hits	Search Text
36	S36	20	"9301288"
37	S37	27	Strittmatter-Stephen-M.in.
38	S38	26	lee-Daniel-h-s.in.
39	S39	14	li-weiwei.in.
40	S40	21	(("3817837") or ("3850752") or ("3939350") or ("3996345") or ("4275149") or ("4277437") or ("4366241") or ("4399216") or ("4510245") or ("4634665") or ("4816567") or ("4968615") or ("5168062") or ("5179017") or ("5223409") or ("5886152") or ("6054297") or ("6475753") or ("6627741") or ("6774216")) .PN.